

SEQUENCE LISTING

5 (1) GENERAL INFORMATION

(i) APPLICANT: Burnham, Martin K.

10 (ii) TITLE OF THE INVENTION: NOVEL XANTHINE PHOSPHORIBOSYL
TRANSFERASE

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Dechert Price & Rhoads

(B) STREET: 997 Lenox Drive, Building 3, Suite 210

(C) CITY: Lawrenceville

(D) STATE: NJ

(E) COUNTRY: USA

20 (F) ZIP: 08543

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

25 (C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

30 (B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bloom, Allen

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(B) REGISTRATION NUMBER: 29,135

(C) REFERENCE/DOCKET NUMBER:

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 609-520-3214

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(B) TELEFAX: 609-520-3259

(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 582 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ATGAAATTAT TAGAAGAGCG CATCCTCAAG GATGGGCATA TCTTGGGTGA
TAACATCCTC 60

AAGGTAGATT CCTTTTAAAC CCACCAAGTT GACTTTAGCT TGATGCGAGA
GATTGGTAAG 120

GTTTTTGCGG AAAAATTTGC TGCTACTGGC ATTACCAAGG TCGTAACCAT
TGAAGCGTCG 180

5 GGTATTGCCC CAGCCGTTTT TACAGCTGAA GCCTTAAACG TTCCCATGAT
TTTCGCCAAA 240

AAAGCTAAGA ACATCACCAT GAACGAAGGC ATCTTAACTG CTCAAGTCTA
CTCCTTTACC 300

AAGCAGGTGA CCAGCACTGT TTCTATCGCT GGAAAATTCC TCTCACCAGA
10 GGACAAGGTT 360

TTGATTATCG ACGATTTTCCT TGCTAATGGC CAAGCTGCTA AAGGCTTGAT
TCAAATCATC 420

GAACAGGCCG GTGCCACAGT CCAAGCTATC GGTATCGTGA TTGAGAAATC
CTTCCAAGAT 480

15 GGTCGTGATT TGCTTGAAAA AGCAGGCTAC CCTGTCCTAT CACTTGCTCG
CTTGGATCGT 540

TTTGAAAATG GTCAGGTCGT ATTTAAGGAG GCAGATCTCT AA
582

20 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Lys Leu Leu Glu Glu Arg Ile Leu Lys Asp Gly His Ile Leu Gly

1 5 10 15
 Asp Asn Ile Leu Lys Val Asp Ser Phe Leu Thr His Gln Val Asp Phe
 20 25 30
 Ser Leu Met Arg Glu Ile Gly Lys Val Phe Ala Glu Lys Phe Ala Ala
 5 35 40 45
 Thr Gly Ile Thr Lys Val Val Thr Ile Glu Ala Ser Gly Ile Ala Pro
 50 55 60
 Ala Val Phe Thr Ala Glu Ala Leu Asn Val Pro Met Ile Phe Ala Lys
 65 70 75 80
 10 Lys Ala Lys Asn Ile Thr Met Asn Glu Gly Ile Leu Thr Ala Gln Val
 85 90 95
 Tyr Ser Phe Thr Lys Gln Val Thr Ser Thr Val Ser Ile Ala Gly Lys
 100 105 110
 Phe Leu Ser Pro Glu Asp Lys Val Leu Ile Ile Asp Asp Phe Leu Ala
 15 115 120 125
 Asn Gly Gln Ala Ala Lys Gly Leu Ile Gln Ile Ile Glu Gln Ala Gly
 130 135 140
 Ala Thr Val Gln Ala Ile Gly Ile Val Ile Glu Lys Ser Phe Gln Asp
 145 150 155 160
 20 Gly Arg Asp Leu Leu Glu Lys Ala Gly Tyr Pro Val Leu Ser Leu Ala
 165 170 175
 Arg Leu Asp Arg Phe Glu Asn Gly Gln Val Val Phe Lys Glu Ala Asp
 180 185 190
 Leu
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 30 **(A) LENGTH:** 579 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAAATTAT TAGAAGAGCG CATCCTCAAG GATGGGCATA TCTTGGGTGA
TAACATCCTC 60
AAGGTAGATT CCTTTTAAAC CCACCAAGTT GACTTTAGCT TGATGCGAGA
10 GATTGGTAAG 120
GTTTTTGCGG AAAAATTTGC TGCTACTGGC ATTACCAAGG TCGTAACCAT
TGAAGCGTCG 180
GGTATTGCCC CAGCCGTTTT TACAGCTGAA GCCTTAAACG TTCCCATGAT
TTTCGCCAAA 240
15 AAAGCTAAGA ACATCACCAT GAACGAAGGC ATCTTAACTG CTCAAGTCTA
CTCCTTTACC 300
AAGCAGGTGA CCAGCACTGT TTCTATCGCT GGAAAATTCC TCTCACCAGA
GGACAAGGTT 360
TTGATTATCG ACGATTTCCT TGCTAATGGC CAAGCTGCTA AAGGCTTGAT
20 TCAAATCATC 420
GAACAGGCCG GTGCCACAGT CCAAGCTATC GGTATCGTGA TTGAGAAATC
CTTCCAAGAT 480
GGTCGTGATT TGCTTGAAAA AGCAGGCTAC CCTGTCCTAT CACTTGCTCG
CTTGGATCGT 540
25 TTTGAAAATG GTCAGGTCGT ATTTAAGGAG GCAGATCTC 579

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Leu Leu Glu Glu Arg Ile Leu Lys Asp Gly His Ile Leu Gly
1 5 10 15
Asp Asn Ile Leu Lys Val Asp Ser Phe Leu Thr His Gln Val Asp Phe
10 20 25 30
Ser Leu Met Arg Glu Ile Gly Lys Val Phe Ala Glu Lys Phe Ala Ala
35 40 45
Thr Gly Ile Thr Lys Val Val Thr Ile Glu Ala Ser Gly Ile Ala Pro
50 55 60
15 Ala Val Phe Thr Ala Glu Ala Leu Asn Val Pro Met Ile Phe Ala Lys
65 70 75 80
Lys Ala Lys Asn Ile Thr Met Asn Glu Gly Ile Leu Thr Ala Gln Val
85 90 95
Tyr Ser Phe Thr Lys Gln Val Thr Ser Thr Val Ser Ile Ala Gly Lys
20 100 105 110
Phe Leu Ser Pro Glu Asp Lys Val Leu Ile Ile Asp Asp Phe Leu Ala
115 120 125
Asn Gly Gln Ala Ala Lys Gly Leu Ile Gln Ile Ile Glu Gln Ala Gly
130 135 140
25 Ala Thr Val Gln Ala Ile Gly Ile Val Ile Glu Lys Ser Phe Gln Asp
145 150 155 160
Gly Arg Asp Leu Leu Glu Lys Ala Gly Tyr Pro Val Leu Ser Leu Ala
165 170 175
Arg Leu Asp Arg Phe Glu Asn Gly Gln Val Val Phe Lys Glu Ala Asp
30 180 185 190
Leu

(2) INFORMATION FOR SEQ ID NO:5:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCCTCAAGGT AGATTCCTTT TTAAC

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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CTCCTTAAAT ACGACCTGAC

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